

Figure 1: Nucleotide (SEQ ID NO: 1) and deduced amino acid sequence of human ChemR23 (AC075748)

1	M	E	D	E	D	Y	N	T	S	I	S	Y	G	D	E	15
175	ATG	GAG	GAT	GAA	GAT	TAC	AAC	ACT	TCC	ATC	AGT	TAC	GGT	GAT	GAA	219
16	Y	P	D	Y	L	D	S	I	V	V	L	E	D	L	S	30
220	TAC	CCT	GAT	TAT	TTA	GAC	TCC	ATT	GTG	GTT	TTG	GAG	GAC	TTA	TCC	264
31	P	L	E	A	R	V	T	R	I	F	L	V	V	V	Y	45
265	CCC	TTG	GAA	GCC	AGG	GTG	ACC	AGG	ATC	TTC	CTG	GTG	GTG	GTC	TAC	309
46	S	I	V	C	F	L	G	I	L	G	N	G	L	V	I	60
310	AGC	ATC	GTC	TGC	TTC	CTC	GGG	ATT	CTG	GGC	AAT	GGT	CTG	GTG	ATC	354
61	I	I	A	T	F	K	M	K	K	T	V	N	M	V	W	75
355	ATC	ATT	GCC	ACC	TTC	AAG	ATG	AAG	AAG	ACA	GTG	AAC	ATG	GTC	TGG	399
76	F	L	N	L	A	V	A	D	F	L	F	N	V	F	L	90
400	TTC	CTC	AAC	CTG	GCA	GTG	GCA	GAT	TTC	CTG	TTC	AAC	GTC	TTC	CTC	444
91	P	I	H	I	T	Y	A	A	M	D	Y	H	W	V	F	105
445	CCA	ATC	CAT	ATC	ACC	TAT	GCC	GCC	ATG	GAC	TAC	CAC	TGG	GTT	TTC	489
106	G	T	A	M	C	K	I	S	N	F	L	L	I	H	N	120
490	GGG	ACA	GCC	ATG	TGC	AAG	ATC	AGC	AAC	TTC	CTT	CTC	ATC	CAC	AAC	534
121	M	F	T	S	V	F	L	L	T	I	I	S	S	D	R	135
535	ATG	TTC	ACC	AGC	GTC	TTC	CTG	CTG	ACC	ATC	ATC	AGC	TCT	GAC	CGC	579
136	C	I	S	V	L	L	P	V	W	S	Q	N	H	R	S	150
580	TGC	ATC	TCT	GTG	CTC	CTC	CCT	GTC	TGG	TCC	CAG	AAC	CAC	CGC	AGC	624
151	V	R	L	A	Y	M	A	C	M	V	I	W	V	L	A	165
625	GTT	CGC	CTG	GCT	TAC	ATG	GCC	TGC	ATG	GTC	ATC	TGG	GTC	CTG	GCT	669
166	F	F	L	S	S	P	S	L	V	F	R	D	T	A	N	180
670	TTC	TTC	TTG	AGT	TCC	CCA	TCT	CTC	GTC	TTC	CGG	GAC	ACA	GCC	AAC	714
181	L	H	G	K	I	S	C	F	N	N	F	S	L	S	T	195
715	CTG	CAT	GGG	AAA	ATA	TCC	TGC	TTC	AAC	AAC	TTC	AGC	CTG	TCC	ACA	759
196	P	G	S	S	S	W	P	T	H	S	Q	M	D	P	V	210
760	CCT	GGG	TCT	TCC	TCG	TGG	CCC	ACT	CAC	TCC	CAA	ATG	GAC	CCT	GTG	804
211	G	Y	S	R	H	M	V	V	T	V	T	R	F	L	C	225
805	GGG	TAT	AGC	CGG	CAC	ATG	GTG	GTG	ACT	GTC	ACC	CGC	TTC	CTC	TGT	849
226	G	F	L	V	P	V	L	I	I	T	A	C	Y	L	T	240
850	GGC	TTC	CTG	GTC	CCA	GTC	CTC	ATC	ATC	ACA	GCT	TGC	TAC	CTC	ACC	894
241	I	V	C	K	L	Q	R	N	R	L	A	K	T	K	K	255
895	ATC	GTC	TGC	AAA	CTG	CAG	CGC	AAC	CGC	CTG	GCC	AAG	ACC	AAG	AAG	939
256	P	F	K	I	I	V	T	I	I	I	T	F	F	L	C	270
940	CCC	TTC	AAG	ATT	ATT	GTG	ACC	ATC	ATC	ATT	ACC	TTC	TTC	CTC	TGC	984

Figure 1: Nucleotide (SEQ ID NO: 1) and deduced amino acid sequence of human ChemR23 (AC075748)

271	W	C	P	Y	H	T	L	N	L	L	E	L	H	H	T	285
985	TGG	TGC	CCC	TAC	CAC	ACA	CTC	AAC	CTC	CTA	GAG	CTC	CAC	CAC	ACT	1029
286	A	M	P	G	S	V	F	S	L	G	L	P	L	A	T	300
1030	GCC	ATG	CCT	GGC	TCT	GTC	TTC	AGC	CTG	GGT	TTG	CCC	CTG	GCC	ACT	1074
301	A	L	A	I	A	N	S	C	M	N	P	I	L	Y	V	315
1075	GCC	CTT	GCC	ATT	GCC	AAC	AGC	TGC	ATG	AAC	CCC	ATT	CTG	TAT	GTT	1119
316	F	M	G	Q	D	F	K	K	F	K	V	A	L	F	S	330
1120	TTC	ATG	GGT	CAG	GAC	TTC	AAG	AAG	TTC	AAG	GTG	GCC	CTC	TTC	TCT	1164
331	R	L	V	N	A	L	S	E	D	T	G	H	S	S	Y	345
1165	CGC	CTG	GTC	AAT	GCT	CTA	AGT	GAA	GAT	ACA	GGC	CAC	TCT	TCC	TAC	1209
346	P	S	H	R	S	F	T	K	M	S	S	M	N	E	R	360
1210	CCC	AGC	CAT	AGA	AGC	TTT	ACC	AAG	ATG	TCA	TCA	ATG	AAT	GAG	AGG	1254
361	T	S	M	N	E	R	E	T	G	M	L	*				372
1255	ACT	TCT	ATG	AAT	GAG	AGG	GAG	ACC	GGC	ATG	CTT	TGA				1290

TTT.D"EE5050

Figure 2: Amino acid sequence of human ChemR23 (371 amino acids) (SEQ ID NO 2). The seven predicted transmembrane domaines are underlined. The consensus sequence for *N*-linked glycosylation (N-X-S/T) in the N terminus is bold and the potential site of phosphorylation by PKC (S/T-X-R/K) in the C terminus is in italic.

MEDEDYNTSISYGDEYPDYLD SIVVLEDLSPLEARVTRIFLVVVYSIVCFLGILGNGLV IIIAT
FKMKKTVMVWFLNLAVADFLFNVFLPIHITYAAMDYHWWFGTAMCKISNFLLIHNMFTSVFLL
TIISSDRCISVLLPVWSQNHRSVRLAYMACMVIWVLAFFLSSPSLVFRDTANLHGKISCFNNFS
LSTPGSSSWPTHSQMDPVGYSRHMVVTVTRFLCGFLVPVLIITACYLTIVCKLQRNRLAKTKKP
FKIIVTIIITFFLCWCPYHTLNLLLELHHTAMPGSVFSLGLPLATALAIANSCMNPILYVFMGQD
FKKFKVALFSRLVNALSEDTGHSSYP SHRSFTKMSSMNERTSMNERETGML

FIG. 2. Amino acid sequence of human ChemR23 (371 amino acids) (SEQ ID NO 2).

Figure 3: Nucleotide and deduced amino acid sequence of mouse dez (AC u79525 – SEQ ID NOs:3 and 4, respectively)

1	M	E	Y	D	A	Y	N	D	S	G	I	Y	D	D	E	15
265	ATG	GAG	TAC	GAC	GCT	TAC	AAC	GAC	TCC	GGC	ATC	TAT	GAT	GAT	GAG	309
16	Y	S	D	G	F	G	Y	F	V	D	L	E	E	A	S	30
310	TAC	TCT	GAT	GGC	TTT	GGC	TAC	TTT	GTG	GAC	TTG	GAG	GAG	GCG	AGT	354
31	P	W	E	A	K	V	A	P	V	F	L	V	V	I	Y	45
355	CCG	TGG	GAG	GCC	AAG	GTG	GCC	CCG	GTC	TTC	CTG	GTG	GTG	ATC	TAC	399
46	S	L	V	C	F	L	G	L	L	G	N	G	L	V	I	60
400	AGC	TTG	GTG	TGC	TTC	CTC	GGT	CTC	CTA	GGC	AAC	GGC	CTG	GTG	ATT	444
61	V	I	A	T	F	K	M	K	K	T	V	N	T	V	W	75
445	GTC	ATC	GCC	ACC	TTC	AAG	ATG	AAG	AAG	ACC	GTG	AAC	ACT	GTG	TGG	489
76	F	V	N	L	A	V	A	D	F	L	F	N	I	F	L	90
490	TTT	GTC	AAC	CTG	GCT	GTG	GCC	GAC	TTC	CTG	TTC	AAC	ATC	TTT	TTG	534
91	P	M	H	I	T	Y	A	A	M	D	Y	H	W	V	F	105
535	CCG	ATG	CAC	ATC	ACC	TAC	GCG	GCC	ATG	GAC	TAC	CAC	TGG	GTG	TTC	579
106	G	K	A	M	C	K	I	S	N	F	L	L	S	H	N	120
580	GGG	AAG	GCC	ATG	TGC	AAG	ATC	AGC	AAC	TTC	TTG	CTC	AGC	CAC	AAC	624
121	M	Y	T	S	V	F	L	L	T	V	I	S	F	D	R	135
625	ATG	TAC	ACC	AGC	GTC	TTC	CTG	CTG	ACT	GTC	ATC	AGC	TTT	GAC	CGC	669
136	C	I	S	V	L	L	P	V	W	S	Q	N	H	R	S	150
670	TGC	ATC	TCC	GTG	CTG	CTC	CCC	GTC	TGG	TCC	CAG	AAC	CAC	CGC	AGC	714
151	I	R	L	A	Y	M	T	C	S	A	V	W	V	L	A	165
715	ATC	CGC	CTG	GCC	TAC	ATG	ACC	TGC	TCG	GCC	GTC	TGG	GTC	CTG	GCT	759
166	F	F	L	S	S	P	S	L	V	F	R	D	T	A	N	180
760	TTC	TTC	TTG	AGC	TCC	CCG	TCC	CTT	GTC	TTC	CGG	GAC	ACC	GCC	AAC	804
181	I	H	G	K	I	T	C	F	N	N	F	S	L	A	A	195
805	ATT	CAT	GGG	AAG	ATA	ACC	TGC	TTC	AAC	AAC	TTC	AGC	TTG	GCC	GCG	849
196	P	E	S	S	P	H	P	A	H	S	Q	V	V	S	T	210
850	CCT	GAG	TCC	TCC	CCA	CAT	CCC	GCC	CAC	TCG	CAA	GTA	GTT	TCC	ACA	894
211	G	Y	S	R	H	V	A	V	T	V	T	R	F	L	C	225
895	GGG	TAC	AGC	AGA	CAC	GTG	GCG	GTC	ACT	GTC	ACC	CGC	TTC	CTT	TGC	939
226	G	F	L	I	P	V	F	I	I	T	A	C	Y	L	T	240
940	GGC	TTC	CTG	ATC	CCC	GTC	TTC	ATC	ATC	ACG	GCC	TGC	TAC	CTT	ACC	984
241	I	V	F	K	L	Q	R	N	R	L	A	K	N	K	K	255
985	ATC	GTC	TTC	AAG	CTG	CAG	CGC	AAC	CGC	CTG	GCC	AAG	AAC	AAG	AAG	1029
256	P	F	K	I	I	I	T	I	I	I	T	F	F	L	C	270
1030	CCC	TTC	AAG	ATC	ATC	ATC	ACC	ATC	ATC	ATC	ACC	TTC	TTC	CTC	TGC	1074
271	W	C	P	Y	H	T	L	Y	L	L	E	L	H	H	T	285
1075	TGG	TGC	CCC	TAC	CAC	ACC	CTC	TAC	CTG	CTG	GAG	CTC	CAC	CAC	ACA	1119
286	A	V	P	S	S	V	F	S	L	G	L	P	L	A	T	300
1120	GCT	GTG	CCA	AGC	TCT	GTC	TTC	AGC	CTG	GGG	CTA	CCC	CTG	GCC	ACG	1164

301	A	V	A	I	A	N	S	C	M	N	P	I	L	Y	V	315
1165	GCC	GTC	GCC	ATC	GCC	AAC	AGC	TGC	ATG	AAC	CCC	ATT	CTG	TAC	GTC	1209
316	F	M	G	H	D	F	R	K	F	K	V	A	L	F	S	330
1210	TTC	ATG	GGC	CAC	GAC	TTC	AGA	AAA	TTC	AAG	GTG	GCC	CTC	TTC	TCC	1254
331	R	L	A	N	A	L	S	E	D	T	G	P	S	S	Y	345
1255	CGC	CTG	GCC	AAC	GCC	CTG	AGT	GAG	GAC	ACA	GGC	CCC	TCC	TCC	TAC	1299
346	P	S	H	R	S	F	T	K	M	S	S	L	N	E	K	360
1300	CCC	AGT	CAC	AGG	AGC	TTC	ACC	AAG	ATG	TCG	TCT	TTG	AAT	GAG	AAG	1344
361	A	S	V	N	E	K	E	T	S	T	L	*				372
1345	GCT	TCG	GTG	AAT	GAG	AAG	GAG	ACC	AGT	ACC	CTC	TGA				1380

Table 1

Parameter	Value
Initial concentration of polymer solution (C_0)	0.01 g/dl
Temperature of solution (T_s)	25 °C
Time of exposure (t)	1 h
Distance between electrodes (d)	1 cm
Voltage applied (V)	10 kV
Area of electrode (A)	1 cm ²
Volume of solution (V_s)	1 ml
Conductivity of solution (κ)	0.01 S/cm
Dielectric constant of solution (ϵ_r)	80
Viscosity of solution (η)	0.01 Pa·s
Density of solution (ρ)	1.0 g/cm ³
Electrode material	Aluminum
Electrode surface area	1 cm ²
Electrode separation	1 cm
Electrode voltage	10 kV
Electrode current	1 mA
Electrode frequency	1 kHz
Electrode waveform	Sine wave
Electrode shape	Rectangular
Electrode thickness	0.1 mm
Electrode width	1 cm
Electrode height	1 cm
Electrode weight	0.1 g
Electrode volume	0.1 cm ³
Electrode density	1.0 g/cm ³
Electrode conductivity	0.01 S/cm
Electrode dielectric constant	80
Electrode viscosity	0.01 Pa·s
Electrode density	1.0 g/cm ³

Figure 4: Nucleotide and deduced amino acid sequence of rat G-protein coupled chemoattractant-1 (AC NM_022218 - SEQ ID Nos: 5 and 6, respectively).

1	M	E	Y	E	G	Y	N	D	S	S	I	Y	G	E	E	15
1	ATG	GAG	TAC	GAG	GGT	TAC	AAC	GAC	TCC	AGC	ATC	TAC	GGT	GAG	GAG	45
16	Y	S	D	G	S	D	Y	I	V	D	L	E	E	A	G	30
46	TAT	TCT	GAC	GGC	TCG	GAC	TAC	ATC	GTG	GAC	TTG	GAG	GAG	GCG	GGT	90
31	P	L	E	A	K	V	A	E	V	F	L	V	V	I	Y	45
91	CCA	CTG	GAG	GCC	AAG	GTG	GCC	GAG	GTC	TTC	CTG	GTG	GTA	ATC	TAC	135
46	S	L	V	C	F	L	G	I	L	G	N	G	L	V	I	60
136	AGC	TTG	GTG	TGC	TTC	CTC	GGG	ATC	CTA	GGC	AAT	GGC	CTG	GTG	ATT	180
61	V	I	A	T	F	K	M	K	K	T	V	N	T	V	W	75
181	GTC	ATC	GCC	ACC	TTC	AAG	ATG	AAG	AAG	ACG	GTG	AAC	ACC	GTG	TGG	225
76	F	V	N	L	A	V	A	D	F	L	F	N	I	F	L	90
226	TTT	GTC	AAC	CTG	GCC	GTG	GCT	GAC	TTC	CTG	TTC	AAC	ATC	TTC	TTG	270
91	P	I	H	T	Y	A	A	M	D	Y	H	W	V	F		105
271	CCC	ATC	CAC	ATC	ACC	TAT	GCC	GCT	ATG	GAC	TAC	CAC	TGG	GTG	TTC	315
106	G	K	A	M	C	K	I	S	S	F	L	L	S	H	N	120
316	GGG	AAA	GCC	ATG	TGC	AAG	ATT	AGT	AGC	TTT	CTG	CTA	AGC	CAC	AAC	360
121	M	Y	T	S	V	F	L	L	T	V	I	S	F	D	R	135
361	ATG	TAC	ACC	AGC	GTC	TTC	CTG	CTC	ACT	GTC	ATC	AGC	TTC	GAC	CGC	405
136	C	I	S	V	L	L	P	V	W	S	Q	N	H	R	S	150
406	TGC	ATC	TCC	GTG	CTC	CTC	CCC	GTC	TGG	TCC	CAG	AAC	CAC	CGC	AGC	450
151	V	R	L	A	Y	M	T	C	V	V	V	W	V	W	L	165
451	GTG	CGT	CTG	GCC	TAC	ATG	ACC	TGC	GTG	GTT	GTC	TGG	GTC	TGG	CTT	495
166	S	S	E	S	P	P	S	L	V	F	G	H	V	S	T	180
496	TCT	TCT	GAG	TCT	CCC	CCG	TCC	CTC	GTC	TTC	GGA	CAC	GTC	AGC	ACC	540
181	S	H	G	K	I	T	C	F	N	N	F	S	L	A	A	195
541	AGC	CAC	GGG	AAG	ATA	ACC	TGC	TTC	AAC	AAC	TTC	AGC	CTG	GCG	GCG	585
196	P	E	P	F	S	H	S	T	H	P	R	T	D	P	V	210
586	CCC	GAG	CCT	TTC	TCT	CAT	TCC	ACC	CAC	CCG	CGA	ACA	GAC	CCG	GTA	630
211	G	Y	S	R	H	V	A	V	T	V	T	R	F	L	C	225
631	GGG	TAC	AGC	AGA	CAT	GTG	GCG	GTC	ACC	GTC	ACC	CGC	TTC	CTC	TGT	675
226	G	F	L	I	P	V	F	I	I	T	A	C	Y	L	T	240
676	GGC	TTC	CTG	ATC	CCC	GTC	TTC	ATC	ATC	ACG	GCC	TGT	TAC	CTC	ACC	720
241	I	V	F	K	L	Q	R	N	R	Q	A	K	T	K	K	255
721	ATC	GTC	TTC	AAG	TTG	CAG	CGC	AAC	CGC	CAG	GCC	AAG	ACC	AAG	AAG	765
256	P	F	K	I	I	I	T	I	I	I	T	F	F	L	C	270
766	CCC	TTC	AAG	ATC	ATC	ATC	ACC	ATC	ATC	ATC	ACC	TTC	TTC	CTC	TGC	810
271	W	C	P	Y	H	T	L	Y	L	L	E	L	H	H	T	285
811	TGG	TGC	CCC	TAC	CAC	ACA	CTC	TAC	CTG	CTG	GAG	CTC	CAC	CAC	ACG	855
286	A	V	P	A	S	V	F	S	L	G	L	P	L	A	T	300

856	GCT	GTG	CCA	GCC	TCT	GTC	TTC	AGC	CTG	GGA	CTG	CCC	CTG	GCC	ACA	900
301	A	V	A	I	A	N	S	C	M	N	P	I	L	Y	V	315
901	GCC	GTC	GCC	ATC	GCC	AAC	AGC	TGT	ATG	AAC	CCC	ATC	CTG	TAC	GTC	945
316	F	M	G	H	D	F	K	K	F	K	V	A	L	F	S	330
946	TTC	ATG	GGC	CAC	GAC	TTC	AAA	AAA	TTC	AAG	GTG	GCC	CTT	TTC	TCC	990
331	R	L	V	N	A	L	S	E	D	T	G	P	S	S	Y	345
991	CGC	CTG	GTG	AAT	GCC	CTG	AGC	GAG	GAC	ACA	GGA	CCC	TCC	TCC	TAC	1035
346	P	S	H	R	S	F	T	K	M	S	S	L	I	E	K	360
1036	CCC	AGT	CAC	AGG	AGC	TTC	ACC	AAG	ATG	TCC	TCA	TTG	ATT	GAG	AAG	1080
361	A	S	V	N	E	K	E	T	S	T	L	*				372
1081	GCT	TCA	GTG	AAT	GAG	AAA	GAG	ACC	AGC	ACC	CTC	TGA				1116

1081 1080 1079 1078 1077 1076 1075 1074 1073 1072 1071 1070 1069 1068 1067 1066 1065 1064 1063 1062 1061 1060 1059 1058 1057 1056 1055 1054 1053 1052 1051 1050 1049 1048 1047 1046 1045 1044 1043 1042 1041 1040 1039 1038 1037 1036 1035 1034 1033 1032 1031 1030 1029 1028 1027 1026 1025 1024 1023 1022 1021 1020 1019 1018 1017 1016 1015 1014 1013 1012 1011 1010 1009 1008 1007 1006 1005 1004 1003 1002 1001 1000 999 998 997 996 995 994 993 992 991 990 989 988 987 986 985 984 983 982 981 980 979 978 977 976 975 974 973 972 971 970 969 968 967 966 965 964 963 962 961 960 959 958 957 956 955 954 953 952 951 950 949 948 947 946 945 944 943 942 941 940 939 938 937 936 935 934 933 932 931 930 929 928 927 926 925 924 923 922 921 920 919 918 917 916 915 914 913 912 911 910 909 908 907 906 905 904 903 902 901 900 899 898 897 896 895 894 893 892 891 890 889 888 887 886 885 884 883 882 881 880 879 878 877 876 875 874 873 872 871 870 869 868 867 866 865 864 863 862 861 860 859 858 857 856 855 854 853 852 851 850 849 848 847 846 845 844 843 842 841 840 839 838 837 836 835 834 833 832 831 830 829 828 827 826 825 824 823 822 821 820 819 818 817 816 815 814 813 812 811 810 809 808 807 806 805 804 803 802 801 800 799 798 797 796 795 794 793 792 791 790 789 788 787 786 785 784 783 782 781 780 779 778 777 776 775 774 773 772 771 770 769 768 767 766 765 764 763 762 761 760 759 758 757 756 755 754 753 752 751 750 749 748 747 746 745 744 743 742 741 740 739 738 737 736 735 734 733 732 731 730 729 728 727 726 725 724 723 722 721 720 719 718 717 716 715 714 713 712 711 710 709 708 707 706 705 704 703 702 701 700 699 698 697 696 695 694 693 692 691 690 689 688 687 686 685 684 683 682 681 680 679 678 677 676 675 674 673 672 671 670 669 668 667 666 665 664 663 662 661 660 659 658 657 656 655 654 653 652 651 650 649 648 647 646 645 644 643 642 641 640 639 638 637 636 635 634 633 632 631 630 629 628 627 626 625 624 623 622 621 620 619 618 617 616 615 614 613 612 611 610 609 608 607 606 605 604 603 602 601 600 599 598 597 596 595 594 593 592 591 590 589 588 587 586 585 584 583 582 581 580 579 578 577 576 575 574 573 572 571 570 569 568 567 566 565 564 563 562 561 560 559 558 557 556 555 554 553 552 551 550 549 548 547 546 545 544 543 542 541 540 539 538 537 536 535 534 533 532 531 530 529 528 527 526 525 524 523 522 521 520 519 518 517 516 515 514 513 512 511 510 509 508 507 506 505 504 503 502 501 500 499 498 497 496 495 494 493 492 491 490 489 488 487 486 485 484 483 482 481 480 479 478 477 476 475 474 473 472 471 470 469 468 467 466 465 464 463 462 461 460 459 458 457 456 455 454 453 452 451 450 449 448 447 446 445 444 443 442 441 440 439 438 437 436 435 434 433 432 431 430 429 428 427 426 425 424 423 422 421 420 419 418 417 416 415 414 413 412 411 410 409 408 407 406 405 404 403 402 401 400 399 398 397 396 395 394 393 392 391 390 389 388 387 386 385 384 383 382 381 380 379 378 377 376 375 374 373 372 371 370 369 368 367 366 365 364 363 362 361 360 359 358 357 356 355 354 353 352 351 350 349 348 347 346 345 344 343 342 341 340 339 338 337 336 335 334 333 332 331 330 329 328 327 326 325 324 323 322 321 320 319 318 317 316 315 314 313 312 311 310 309 308 307 306 305 304 303 302 301 300 299 298 297 296 295 294 293 292 291 290 289 288 287 286 285 284 283 282 281 280 279 278 277 276 275 274 273 272 271 270 269 268 267 266 265 264 263 262 261 260 259 258 257 256 255 254 253 252 251 250 249 248 247 246 245 244 243 242 241 240 239 238 237 236 235 234 233 232 231 230 229 228 227 226 225 224 223 222 221 220 219 218 217 216 215 214 213 212 211 210 209 208 207 206 205 204 203 202 201 200 199 198 197 196 195 194 193 192 191 190 189 188 187 186 185 184 183 182 181 180 179 178 177 176 175 174 173 172 171 170 169 168 167 166 165 164 163 162 161 160 159 158 157 156 155 154 153 152 151 150 149 148 147 146 145 144 143 142 141 140 139 138 137 136 135 134 133 132 131 130 129 128 127 126 125 124 123 122 121 120 119 118 117 116 115 114 113 112 111 110 109 108 107 106 105 104 103 102 101 100 99 98 97 96 95 94 93 92 91 90 89 88 87 86 85 84 83 82 81 80 79 78 77 76 75 74 73 72 71 70 69 68 67 66 65 64 63 62 61 60 59 58 57 56 55 54 53 52 51 50 49 48 47 46 45 44 43 42 41 40 39 38 37 36 35 34 33 32 31 30 29 28 27 26 25 24 23 22 21 20 19 18 17 16 15 14 13 12 11 10 9 8 7 6 5 4 3 2 1 0

Figure 5: Alignment of ChemR23

Alignment of the amino acid sequence of ChemR23 with AT2 receptors, C3a, C5a and fMLP receptor and other chemoattractants related sequences were performed using ClustalX algorithm. Then, the dendrogram was constructed using TreeView algorithm.

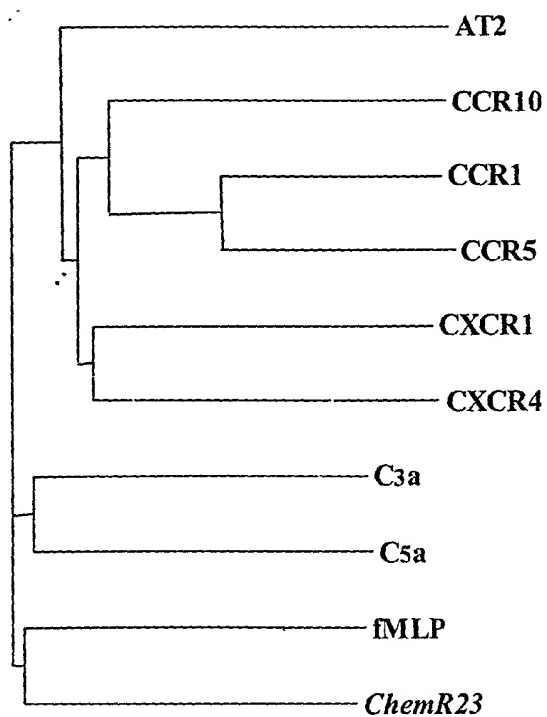


Figure 6: Nucleotide and deduced amino acid sequence of human Tig2 (AC Q99969 - SEQ ID Nos: 7 and 8, respectively)

1	M	R	R	L	L	I	P	L	A	L	W	L	G	A	V	15
97	ATG	CGA	CGG	CTG	CTG	ATC	CCT	CTG	GCC	CTG	TGG	CTG	GGT	GCG	GTG	141
16	G	V	G	V	A	E	L	T	E	A	Q	R	R	G	L	30
142	GGC	GTG	GGC	GTC	GCC	GAG	CTC	ACG	GAA	GCC	CAG	CGC	CGG	GGC	CTG	186
31	Q	V	A	L	E	E	F	H	K	H	P	P	V	Q	W	45
187	CAG	GTG	GCC	CTG	GAG	GAA	TTT	CAC	AAG	CAC	CCG	CCC	GTG	CAG	TGG	231
46	A	F	Q	E	T	S	V	E	S	A	V	D	T	P	F	60
232	GCC	TTC	CAG	GAG	ACC	AGT	GTG	GAG	AGC	GCC	GTG	GAC	ACG	CCC	TTC	276
61	P	A	G	I	F	V	R	L	E	F	K	L	Q	Q	T	75
277	CCA	GCT	GGA	ATA	TTT	GTG	AGG	CTG	GAA	TTT	AAG	CTG	CAG	CAG	ACA	321
76	S	C	R	K	R	D	W	K	K	P	E	C	K	V	R	90
322	AGC	TGC	CGG	AAG	AGG	GAC	TGG	AAG	AAA	CCC	GAG	TGC	AAA	GTC	AGG	366
91	P	N	G	R	K	R	K	C	L	A	C	I	K	L	G	105
367	CCC	AAT	GGG	AGG	AAA	CGG	AAA	TGC	CTG	GCC	TGC	ATC	AAA	CTG	GGC	411
106	S	E	D	K	V	L	G	R	L	V	H	C	P	I	E	120
412	TCT	GAG	GAC	AAA	GTT	CTG	GGC	CGG	TTG	GTC	CAC	TGC	CCC	ATA	GAG	456
121	T	Q	V	L	R	E	A	E	E	H	Q	E	T	Q	C	135
457	ACC	CAA	GTT	CTG	CGG	GAG	GCT	GAG	GAG	CAC	CAG	GAG	ACC	CAG	TGC	501
136	L	R	V	Q	R	A	G	E	D	P	H	S	F	Y	F	150
502	CTC	AGG	GTG	CAG	CGG	GCT	GGT	GAG	GAC	CCC	CAC	AGC	TTC	TAC	TTC	546
151	P	G	Q	F	A	F	S	K	A	L	P	R	S	*		164
547	CCT	GGA	CAG	TTC	GCC	TTC	TCC	AAG	GCC	CTG	CCC	CGC	AGC	TAA		588

099099-0744

Figure 7: Nucleotide and deduced amino acid sequence of mouse Tig2
(SEQ ID Nos: 9 and 10, respectively)

1	M	K	C	L	L	I	S	L	A	L	W	L	G	T	V	15
102	ATG	AAG	TGC	TTG	CTG	ATC	TCC	CTA	GCC	CTA	TGG	CTG	GGC	ACA	GTG	146
16	G	T	R	G	T	E	P	E	L	S	E	T	Q	R	R	30
147	GGC	ACA	CGT	GGG	ACA	GAG	CCC	GAA	CTC	AGC	GAG	ACC	CAG	CGC	AGG	191
31	S	L	Q	V	A	L	E	E	F	H	K	H	P	P	V	45
192	AGC	CTA	CAG	GTG	GCT	CTG	GAG	GAG	TTC	CAC	AAA	CAC	CCA	CCT	GTG	236
46	Q	L	A	F	Q	E	I	G	V	D	R	A	E	E	V	60
237	CAG	TTG	GCC	TTC	CAA	GAG	ATC	GGT	GTG	GAC	AGA	GCT	GAA	GAA	GTG	281
61	L	F	S	A	G	T	F	V	R	L	E	F	K	L	Q	75
282	CTC	TTC	TCA	GCT	GGC	ACC	TTT	GTG	AGG	TTG	GAA	TTT	AAG	CTC	CAG	326
76	Q	T	N	C	P	K	K	D	W	K	K	P	E	C	T	90
327	CAG	ACC	AAC	TGC	CCC	AAG	AAG	GAC	TGG	AAA	AAG	CCG	GAG	TGC	ACA	371
91	I	K	P	N	G	R	R	R	K	C	L	A	C	I	K	105
372	ATC	AAA	CCA	AAC	GGG	AGA	AGG	CGG	AAA	TGC	CTG	GCC	TGC	ATT	AAA	416
106	M	D	P	K	C	K	I	L	G	R	I	V	H	C	P	120
417	ATG	GAC	CCC	AAG	GGT	AAA	ATT	CTA	GGC	CGG	ATA	GTC	CAC	TGC	CCA	461
121	I	L	K	Q	G	P	Q	D	P	Q	E	L	Q	C	I	135
492	ATT	CTG	AAG	CAA	GGG	CCT	CAG	GAT	CCT	CAG	GAG	TTG	CAA	TGC	ATT	506
136	K	I	A	Q	A	G	E	D	P	H	G	Y	F	L	P	150
507	AAG	ATA	GCA	CAG	GCT	GGC	GAA	GAC	CCC	CAC	GGC	TAC	TTC	CTA	CCT	551
151	G	Q	F	A	F	S	R	A	L	R	T	K	*			163
552	GGA	CAG	TTT	GCC	TTC	TCC	AGG	GCC	CTG	AGA	ACC	AAA	TAA			590

FIG. 7

Year	1950	1951	1952	1953	1954	1955	1956	1957	1958	1959	1960	1961	1962	1963	1964	1965	1966	1967	1968	1969	1970	1971	1972	1973	1974	1975	1976	1977	1978	1979	1980	1981	1982	1983	1984	1985	1986	1987	1988	1989	1990	1991	1992	1993	1994	1995	1996	1997	1998	1999	2000	2001	2002	2003	2004	2005	2006	2007	2008	2009	2010	2011	2012	2013	2014	2015	2016	2017	2018	2019	2020	2021	2022	2023	2024	2025	2026	2027	2028	2029	2030	2031	2032	2033	2034	2035	2036	2037	2038	2039	2040	2041	2042	2043	2044	2045	2046	2047	2048	2049	2050	2051	2052	2053	2054	2055	2056	2057	2058	2059	2060	2061	2062	2063	2064	2065	2066	2067	2068	2069	2070	2071	2072	2073	2074	2075	2076	2077	2078	2079	2080	2081	2082	2083	2084	2085	2086	2087	2088	2089	2090	2091	2092	2093	2094	2095	2096	2097	2098	2099	2100																			
Population	1,000,000	1,050,000	1,100,000	1,150,000	1,200,000	1,250,000	1,300,000	1,350,000	1,400,000	1,450,000	1,500,000	1,550,000	1,600,000	1,650,000	1,700,000	1,750,000	1,800,000	1,850,000	1,900,000	1,950,000	2,000,000	2,050,000	2,100,000	2,150,000	2,200,000	2,250,000	2,300,000	2,350,000	2,400,000	2,450,000	2,500,000	2,550,000	2,600,000	2,650,000	2,700,000	2,750,000	2,800,000	2,850,000	2,900,000	2,950,000	3,000,000	3,050,000	3,100,000	3,150,000	3,200,000	3,250,000	3,300,000	3,350,000	3,400,000	3,450,000	3,500,000	3,550,000	3,600,000	3,650,000	3,700,000	3,750,000	3,800,000	3,850,000	3,900,000	3,950,000	4,000,000	4,050,000	4,100,000	4,150,000	4,200,000	4,250,000	4,300,000	4,350,000	4,400,000	4,450,000	4,500,000	4,550,000	4,600,000	4,650,000	4,700,000	4,750,000	4,800,000	4,850,000	4,900,000	4,950,000	5,000,000	5,050,000	5,100,000	5,150,000	5,200,000	5,250,000	5,300,000	5,350,000	5,400,000	5,450,000	5,500,000	5,550,000	5,600,000	5,650,000	5,700,000	5,750,000	5,800,000	5,850,000	5,900,000	5,950,000	6,000,000	6,050,000	6,100,000	6,150,000	6,200,000	6,250,000	6,300,000	6,350,000	6,400,000	6,450,000	6,500,000	6,550,000	6,600,000	6,650,000	6,700,000	6,750,000	6,800,000	6,850,000	6,900,000	6,950,000	7,000,000	7,050,000	7,100,000	7,150,000	7,200,000	7,250,000	7,300,000	7,350,000	7,400,000	7,450,000	7,500,000	7,550,000	7,600,000	7,650,000	7,700,000	7,750,000	7,800,000	7,850,000	7,900,000	7,950,000	8,000,000	8,050,000	8,100,000	8,150,000	8,200,000	8,250,000	8,300,000	8,350,000	8,400,000	8,450,000	8,500,000	8,550,000	8,600,000	8,650,000	8,700,000	8,750,000	8,800,000	8,850,000	8,900,000	8,950,000	9,000,000	9,050,000	9,100,000	9,150,000	9,200,000	9,250,000	9,300,000	9,350,000	9,400,000	9,450,000

60 * 80 * 100 *
 HUMAN : SEVDTPFPAGIFVRLEFKLQQTSCRKRDWKKPECKVRPNGRKRKCLACIKLGSSED : 108
 MOUSE : REEVLESACTFVRLEFKLQQTNCPKKDWWKPECTIKPNGRRRKCLACIKMDPKG : 110

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          120          *          140          *          160
HUMAN : KVLGRLVHCPETQVLREAEEHQETQCLRWQRAGEDPHSYTFPGQFAFSKALPRS : 163
MOUSE : KILGRIVHCPILKQ---GPGDPQELQCIKIAQAGEDPHGYTFLPQFAFSRALRTK : 162

```

151

168

mus HGYFLPGQFA FSRALRTK

rat RIYFFPGQFA FSRAL~~~

tig2 HSFYFPGQFA FSKALPRS

sus HSYFPGQFA FFKALPPS

bos HSYLPGQFA FIKAL~~~

gallus DVLYLPGMFA FSKGLP~~

Identities :

T0472044560

:

	bos.pep	mus.pep	sus.pep	gallus	rat.pep
tig2.pep	83.750	56.250	86.503	30.675	61.392
bos.pep		54.375	87.500	31.875	56.329
mus.pep			54.375	31.677	73.125
sus.pep				31.288	58.228
gallus.pep					30.818

$\begin{Bmatrix} 1 \\ 2 \\ 3 \\ 4 \\ 5 \\ 6 \\ 7 \\ 8 \\ 9 \\ 10 \\ 11 \\ 12 \\ 13 \\ 14 \\ 15 \\ 16 \\ 17 \\ 18 \\ 19 \\ 20 \\ 21 \\ 22 \\ 23 \\ 24 \\ 25 \\ 26 \\ 27 \\ 28 \\ 29 \\ 30 \\ 31 \\ 32 \\ 33 \\ 34 \\ 35 \\ 36 \\ 37 \\ 38 \\ 39 \\ 40 \\ 41 \\ 42 \\ 43 \\ 44 \\ 45 \\ 46 \\ 47 \\ 48 \\ 49 \\ 50 \\ 51 \\ 52 \\ 53 \\ 54 \\ 55 \\ 56 \\ 57 \\ 58 \\ 59 \\ 60 \\ 61 \\ 62 \\ 63 \\ 64 \\ 65 \\ 66 \\ 67 \\ 68 \\ 69 \\ 70 \\ 71 \\ 72 \\ 73 \\ 74 \\ 75 \\ 76 \\ 77 \\ 78 \\ 79 \\ 80 \\ 81 \\ 82 \\ 83 \\ 84 \\ 85 \\ 86 \\ 87 \\ 88 \\ 89 \\ 90 \\ 91 \\ 92 \\ 93 \\ 94 \\ 95 \\ 96 \\ 97 \\ 98 \\ 99 \\ 100 \end{Bmatrix}$

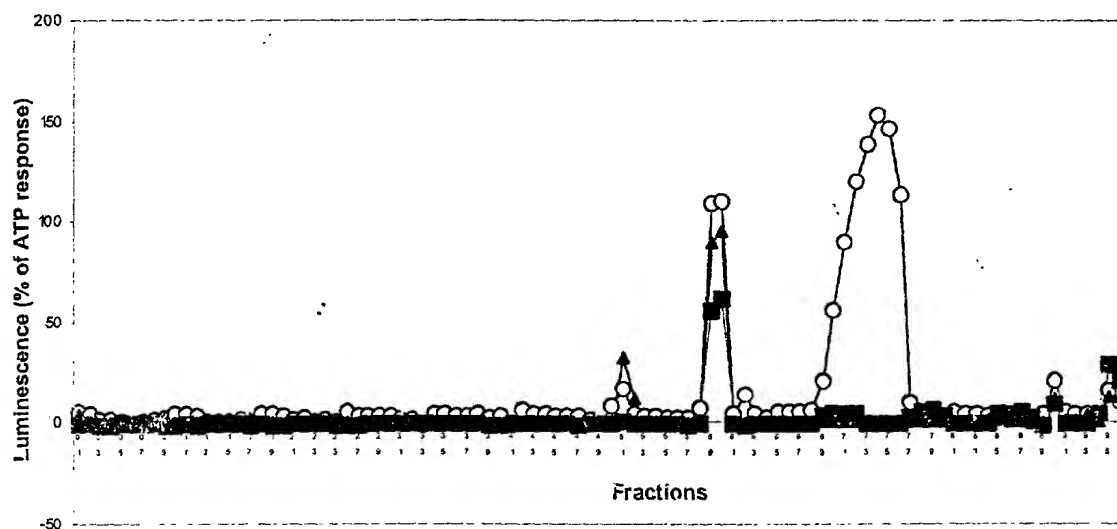
[illegible]

Figure 12: Activation of ChemR23 by cells transfected with TIG2

293 T cells were transiently transfected with pCDNA3- TIG2 or with pCDNA3 alone (mock transfected). Increasing volumes of the supernatant collected 4 days following transfection were analysed in a aequorin-based assay with CHO cells expressing ChemR23. A representative experiment is shown. Assay was performed in triplicate and SD are indicated.

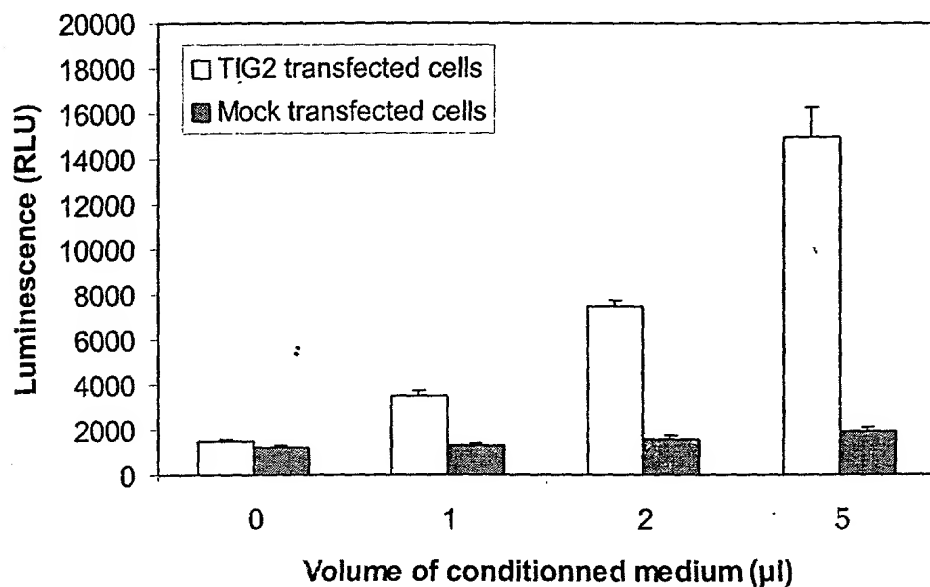


Figure 13: Characterization of antibodies directed against ChemR23

A mixture of recombinant cells made up of 2/3 recombinant ChemR23 CHO cells and 1/3 recombinant HCR CHO cells (negative control) was subject to react with either a supernatant of the anti ChemR23 5C 1H2 monoclonal antibody (thick line) or a supernatant with no known antibody activity (thin line, grey filling). After staining with FITC labeled anti mouse Ig these preparations were analysed by flow cytometry. Results are displayed as a histogram of the number of cells (Events axis) expressing a given fluorescence (FL1-H axis). Monoclonal 5C 1H2 allowed to discriminate the ChemR23 recombinant sub-population of cells from the negative control cells as evidenced by the relative proportions of both type of cells. The background fluorescence of the assay is given by the second staining (grey filling).

